

IN THE SPECIFICATION

Please amend the ninth full paragraph starting on Page 13, line 19 as follows:

Figure 9 depicts an ADP nucleotide SEQ ID NO:17 and amino acid sequence SEQ ID NO:18.

Please delete Table 4 on page 86 in its entirety and replace with the following:

Table 4

Primer	Sequence	Note
A.	5'-GACGTCGACTAATTCCGGTTATTTTCCA SEQ ID NO:19	For PCR EMCV IRES, <i>GTCGAC</i> is a <i>Sal</i> I site.
B.	5'-GACGTCGACATCGTGTTTCAAGGAA SEQ ID NO:20	For PCR EMCV IRES, <i>GTCGAC</i> is a <i>Sal</i> I site.
C.	5'-CCTGAGACGCCCGACATCACCTGTG SEQ ID NO:21	Ad5 sequence to 1314 to 1338.
D.	5'- <u>GTCGACCATT</u> CAGCAAACAAAGGCGTTAAC SEQ ID NO:22	Antisense of Ad5 sequence 1572 to 1586. <i>GTCGAC</i> is a <i>Sal</i> I site. Underline region overlaps with E.
E.	5'- <u>TGCTGAATGGTCGACAT</u> GAGGCTTGGGAG SEQ ID NO:23	Ad5 sequence 1714 to 1728. <i>GTCGAC</i> is a <i>Sal</i> I site. Underline region overlaps with D.
F.	5'-CACAAACCGCTCTCCACAGATGCATG SEQ ID NO:24	Antisense of Ad5 sequence 2070 to 2094.

Please amend the second full paragraph starting on page 90, line 18 as follows:

The 519 base pair EMCV IRES segment was PCR amplified from Novagen's pCITE vector by primers A/B:

primer 1: 5'-GACGTCGACTAATTCCGGTTATTTTCCA SEQ ID NO:19

primer B: 5'GACGTCGACATCGTGTTTTTCAAAGGAA SEQ ID NO:20

(GTCGAC is a SalI site).

Please amend the fourth full paragraph starting on page 91, line 15 as follows:

CP1088

The 2.2kb (-225 to +1) human UPII was amplified from CP657 with primer 127.2.1 (5'AGGACCGGTCACTATAGGGCACGCGTGGT-3' (SEQ ID NO:25)) PLUS 127.2.2 (5'-AGGACCGGTGGGATGCTGGGCTGGGAGGTGG-3' SEQ ID NO:26)) and digested with PinAI and ligated with CP629 cut with PinAI.

Please delete Table 6 in its entirety beginning on page 93, line 16 and ending on page 95, line 3, and replace with the following:

Name	Vector	Ad5 Vector	E1A TRE	E1B TRE	E3
CV874	CP1086	pBHGE3	1.9 kb mUII	IRES	intact
CV875	CP1087	pBHGE3	1.0 kb hUPII	IRES	intact
CV876	CP1088	pBHGE3	2.2 kb hUPII	IRES	intact
CV877	CP1089	pBHGE3	1.0 kb hUPII	1.0 kb hUPII (E1B promoter deleted)	intact
CV882	CP1129	pBHGE3	1.8 kb hUPII	IRES	intact
CV884	CP1131	pBHGE3	1.8kb hUPii	IRES (E1B 19- kDA deleted)	intact

Viruses are tested and characterized as described above.

Primer sequences:

96.74.1	GACGTCGACATCGTCGTTTTCAAAGGAA	SEQ ID NO:20
96.74.2	GACGTCGACTAATTCCGGTTAATTTTCCA	SEQ ID NO:19
96.74.3	CCTGAGACGCCCCGACATCACCTGTG	SEQ ID NO:21
96.74.4	TGCTGAATGGTCGACATGGAGGCTTGGGAG	SEQ ID NO:23
96.74.5	CACAACCGCTCTCCACAGATGCATG	SEQ ID NO:24
96.74.6	GTCGACCATTTCAGCAAACAAAGGCGTTAAC	SEQ ID NO:22
100.113.1	AGGGGTACCCACTATAGGGCACGCGTGGT	SEQ ID NO:27
100.113.2	ACCCAAGCTTGGGATGCTGGGCTGGGAGGTGG	SEQ ID NO:28
127.2.2	AGGACCGGTGGGATGCTGGGCTGGGAGGTGG	SEQ ID NO:26
127.50.1	AGAACCGGTCAGGCTTCACCCCAGACCCAC	SEQ ID NO:29
31.166.1	TGCGCCGGTGTACACAGGAAGTGA	SEQ ID NO:30
32.32.1	GAGTTTGTGCCATCGGTCTAC	SEQ ID NO:31
32.32.2	AATCAATCCTTAGTCCTCCTG	SEQ ID NO:32
51.176	GCAGAAAAATCTTCCAAACACTCCC	SEQ ID NO:33
99.120.1	ACGTACACCGGTCGTTACATAACTTAC	SEQ ID NO:34
99.120.2	CTAGCAACCGGTCGGTTCATAAACG	SEQ ID NO:35